ALLOZYMIC AND scnDNA HOMOGENEITY IN POLAR COD (*BOREOGADUS SAIDA*) (GADIFORMES: GADIDAE) *

by

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ABSTRACT. - Polar cod in the Arctic Ocean exhibits variation over its distributional area in both morphometry, coloration and behaviour. The genetic basis to this variation is not known. Thus, a population genetic survey of polar cod was initiated. Specimens were sampled from the Pechora Sea, off Svalbard and in the Denmark Strait and examined for variation at selected enzyme coding loci plus at a scnDNA locus. None of the assays revealed a genetic structuring among the three geographic regions. Moreover, the predominant nonpolymorphic allozyme loci indicated that the genetic variation in polar cod is in general low, which may be in accordance with other species of fish in arctic regions.

RÉSUMÉ. - Homogénéité allozymique et du locus scnDNA chez *Boreogadus saida* (Gadiformes: Gadidae).

La morue arctique, *Boreogadus saida*, présente des variations, dans toute son aire de distribution, à la fois dans la morphométrie, la coloration et le comportement. L'origine génétique de ces variations n'est pas connue. C'est pourquoi une étude génétique générale de la morue arctique a été entreprise. Des échantillons ont été collectés en Mer Péchora, au large du Svalbard et dans le détroit du Danemark, puis examinés du point de vue de certains loci codant les enzymes et du locus du scnADN. Aucun des essais ne permit de mettre en évidence une différence génétique entre les populations des trois régions. De plus, les loci des allozymes non polymorphes montrèrent que les variations génétiques chez la morue arctique sont généralement faibles, ce qui pourrait aussi être le cas chez les autres espèces de poissons arctiques.

Key-words. - Gadidae, *Boreogadus saida*, PN, Arctic Ocean, Population structure, Allozymes, scnDNA.

Polar cod, *Boreogadus saida* (Gadinae), is the most conspicuous pelagic fish species that inhabits the Arctic Ocean. It is extremely abundant, it occurs seasonally in large shoals (Welch *et al.*, 1993), and it provides an important link between lower trophic levels and its main predators, birds and sea mammals (Rass, 1968; Hobson and Welch, 1992). Polar cod is a small-sized (body length ~ 250 mm) and short-lived (~ 5-7 years) gadoid fish with a coherent circumpolar distribution (Fig. 1). Earlier studies on polar cod distribution and migratory behaviour have been conducted mainly in the Eurasian and Russian regions of the Arctic Ocean (Ponomarenko, 1968). Separate stocks of polar cod have been described from Russian arctic waters with each stock having discrete spawning sites and displaying different times of spawning (Rass, 1968). In the Barents Sea, polar

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cod is known to spawn in large quantities south-west of Novaya Zemlya (Ponomarenko, 1968). It has been anticipated that polar cod also spawns off the Svalbard archipelago, but a recent investigation failed to locate spawning sites in the waters off Svalbard (Melle *et al.*, 1996). This could, however, be due to the fact that the timing of sampling did not coincide with the time of spawning. Thus far, no spawning sites have been identified in North American waters.

Moreover, two distinct types of polar cod have been described from the Laptev, Kara, and Pechora Seas (Kashkina, 1962; Moskalenko, 1964). The types differ in body morphometry and coloration at both the larval (Kashkina, 1962) and adult (Moskalenko, 1964) stages with one type occuring near the coast whereas the other type appears to be associated with open oceanic waters only. The genetic basis related to the behavioural and morphological differences seen in polar cod is, however, not known, and questions related to the genetic population structure have remained to be addressed. Consequently, samples of juvenile and adult polar cod were collected in the Pechora Sea (70°N; 54°E), off the Svalbard archipelago (78°N; 10°E), and in the Denmark Strait (66°N; 28°W) (Fig. 1) for comparisons at the allozyme and DNA level.

RESULTS

Allozymic variation was sought in loci coding for 20 different enzymes (methods as in Fevolden and Ayala, 1981). The following 11 systems were monomorphic in the initial screening and were thus not subject to further examination: adenylate kinase (E.C. number 2.7.4.3; 2 loci), aldehyde oxidase (1.2.3.1; 2 loci), fumarase (4.2.1.2), hexokinase (2.7.1.1), hydroxybutyrate dehydrogenase (1.1.1.30), isocitrate dehydrogenase (1.1.1.27), leucine aminopeptidase (3.4.11), octanol dehydrogenase (2 loci), sorbitol dehydrogenase (1.1.1.14; 3 loci), superoxide dismutase (1.15.1.1), and xanthine dehydrogenase. No interpretational bands were seen in amino aspartate transaminase (2.6.1.1), malic emzyme (1.1.1.40), and lactate dehydrogenase (1.1.1.27), whereas the following six systems were at the initial screening questioned as possibly polymorphic: esterase (4.2.1.11, 2 loci), glucose phosphate isomerase (5.3.1.19; 2 loci), malate dehydrogenase (1.1.1.37), mannose phosphate isomerase (5.3.1.8), phosphoglucomutase (2.7.5.1), and 6-phosphogluconate dehydrogenase (1.1.1.44). Thus, 30 fish from each of the area Svalbard, Pechora Sea and Denmark Strait (Fig. 1) were analyzed for possible intra- and inter-geographic variation at the loci coding for those enzymes. By applying a conservative interpretation of the gel patterns, no heterozygotes were scored among the 90 specimens for any of the loci coding for esterase, GPI, 6PGDH, or PGM. The zymograms of MDH and MPI could not be interpreted with confidence.

One single copy nuclear (scn) DNA restriction length polymorphisms (GM798; Pogson *et al.*, 1995), has been shown to be a highly potential marker to distinguish between populations of Atlantic cod (*Gadus morhua*) (Fevolden and Pogson, 1995, 1997). The gene has now been identified as the cod synaptophysin locus (*Syp*-1) (Fevolden and Pogson, 1997) and seems to be conserved in almost any gadoid species (Pogson, unpubl. data). Primers have been constructed that amplify an intron of the *Syp*-1 gene that is polymorphic for the *Dra*-1 restriction site in cod. Thus, *Syp*-1 was subjected for investigation also in polar cod (methods as in Fevolden and Pogson, 1997). The relatively low number of individuals that have been analyzed (42 from the Pechora Sea, approximately 10 from each of the Svalbard and Denmark Strait samples), have revealed no polymorphism or geograhic variation. All individuals were classified as the same homozygote.

Fig. 1. - Distributional range and sampling sites (black asterix) of *Boreogadus saida*. The four main spawning grounds are shown in black.

CONCLUSION

These preliminary investigations have revealed no genetic structuring of *B. saida*, neither at enzyme coding loci, nor at the scnDNA gene. Moreover, the allozyme data seem to reveal very little genetic variation in the species in general. An investigation is now under progress where possible variation at a number of randomly amplified polymorphic DNA sites (RAPDs) are sought. Moreover, the geographic area has been extended to include waters off the western coast of Greenland (Disko Bay). If those data are supportive of the present data, one must conclude that *B. saida* reveals a low genetic polymorphism, which is comparable to other arctic fish (e.g., Fevolden *et al.*, 1989, and references the-

rein), but may be at odds with data from selected Antarctic fish. Thus, the physiological and morphometric differences reported above, may reflect environmentally phenotypic impact more than being invoked by genetic differences. It is acknowledged, however, that lack of genetic differentiation at the monomorphic loci investigated, does not necessarily imply absence of a breeding structure in polar cod.

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